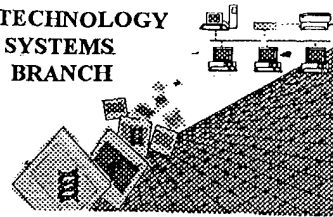


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/675,444
Source: oip
Date Processed by STIC: 10-10-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/675,444
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 X _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/675,444

DATE: 10/10/2003
TIME: 14:38:05

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\10102003\J675444.raw

1 <110> APPLICANT: Giese, Matthias <120> Equine
W--> 2 <130> FILE REFERENCE: Not known yet <160> 61 <170> PatentIn version 3.1
E--> 0 <120> TITLE INVENTION: mandatory response

ERRORED SEQUENCES

Sample of global format errors.

E--> 308 <210> SEQ ID NO: 2<211> 684<212> DNA<213> Artificial Sequence: ORF2 of EAV<400> 2
E--> 309 <211> LENGTH:
E--> 309 <212> TYPE:
E--> 309 <213> ORGANISM:
E--> 309 <400> SEQUENCE:

**Does Not Comply
Corrected Diskette Needed**

*Invalid
response
see item 10
on error
summary
report.*

309 tgctatttct gtgattgatg cagcgctttt ctttctcatg ctacttgcac tggctgttgt 60
311 tactgtgttt cttttctggc tcattgttgc catcggcgcg agcttggtgg cgcggtgttc 120
313 acgaggtgcg cgttacagac ctgtttaagg atttgcagtg cgacaacctg cgcgcgaaag 180
315 atgccttccc gagtctggga tatgctctgt cgattggcca gtcgaggcta tcgtatatgc 240
317 tgcaggattg gttgcttgct gcgcaccgca aggaagtatt gccttccaat atcatgccta 300
319 tgcccggctc tactcctgat tgccttgacc atctggagtc ttctagctat gctccattta 360
321 tcaatgccta tcggcaggca attttgagtc aatacccaca agagctccag ctccaagcca 420
323 tcaactgtaa attgcttgct gtggttgac cggcattgta tcataattac catctagcca 480
325 atttgaccgg accggccaca tgggtcgtgc ctacagtggg ccagttgcac tattatgctt 540
327 cttcctctat ttttgcttca tctgtggaag tgttggcagc aataatacta ctatttgcac 600
329 gcataccact agtgacacga gtgtacatct cttttacgcg gctaattgtca ccttcccgtc 660
331 gcacttccag cggcactttg ccgc 684

E--> 334 <210> SEQ ID NO: 3<211> 501<212> DNA<213> Artificial Sequence: ORF3 of EAV<400> 3

E--> 335 <211> LENGTH:

E--> 335 <212> TYPE:

E--> 335 <213> ORGANISM:

E--> 335 <400> SEQUENCE:

335 accggccaca tgggtcgtgc ctacagtggg ccagttgcac tattatgctt cttcctctat 60
337 ttttgcttca tctgtggaag tgttggcagc aataatacta ctatttgcac gcataccact 120
339 agtgacacga gtgtacatct cttttacgcg gctaattgtca ccttcccgtc gcacttccag 180
341 cggcactttg ccgcggcgca agattttgta gtgcacacgg gttatgaata tgccgggggtc 240
343 actatgttag tgcacttggt tgccaacttg gttctgacat ttccgagctt agttaattgt 300
345 tcccgccttg tgaatgtctt tgctaattgt tcttgcggtg aagtgggttg tagtcatacc 360
347 aactcaacta ctggcttggg tcaactttct ttttcctttg tagatgaaga tctacggctg 420
349 catatcaggc ctactcttat ttgttggtt gccttggtgt tgggtgcactt tctacccatg 480
351 ccacgtgtca gaggtcgtga a 501

E--> 354 <210> SEQ ID NO: 4<211> 458<212> DNA<213> Artificial Sequence: ORF4 of EAV<400> 4

E--> 355 <211> LENGTH:

E--> 355 <212> TYPE:

E--> 355 <213> ORGANISM:

E--> 355 <400> SEQUENCE:

*Please contact Mark Spencer at 703-308-4212
for PatentIn assistance*